Molecular characterization of AI viruses from poultry and wild bird surveillance in Denmark

Larsen, Lars Erik; Krog, Jesper Schak; Madsen, Jesper J.; Thorup, Kasper; Hjulsager, Charlotte Kristiane

Publication date:
2015

Document Version
Publisher's PDF, also known as Version of record

Molecular characterization of AI viruses from poultry and wild bird surveillance in Denmark

Abstract for oral presentation by Charlotte K Hjulsager at 9th International Symposium on Avian Influenza. Athens, Georgia, US. April 12-15, 2015.

Authors: Lars E. Larsen (1); Jesper S. Krog (1), Jesper J. Madsen (2), Kasper Thorup (2) Charlotte K. Hjulsager (1).

National Veterinary Institute, Technical University of Denmark (1), National History Museum of Denmark, Copenhagen University (2).

Abstract

Infection with avian influenza virus (AIV) in poultry may cause devastating disease although the same virus may not cause disease in wild birds. Since AI viruses can be exchanged between poultry and wild birds, surveillance in wild birds provides important knowledge for control of disease in poultry.

AIV's from the Danish wild bird active surveillance were characterized, focusing on viruses from 2012, and from outbreaks of AI in poultry in Denmark. The matrix (M) gene from more than 50 viruses of different subtypes and the hemagglutinin (HA) gene from more than 30 subtype H5 low pathogenic viruses were sequenced and compared by alignment and phylogenetic analyses. The aim was to evaluate: the origin of viruses from outbreaks of AI in Danish poultry, the design of active surveillance in Denmark, and the suitability of the molecular diagnostic RT-PCR tests employed.

All M-genes from Danish viruses grouped phylogenetically with Eurasian lineage viruses. Grouping among Danish sequences was not correlated to place or to the time of sampling within the same year, although there was a tendency to grouping according to the year of sampling. Similar results were observed for H5 sequences.

M and H5/H7 gene sequences from poultry showed a high degree of similarity to Danish wild bird sequences, suggesting exchange of viruses between geographically close wild birds and poultry.

Significant drift was observed in both M and H5 gene sequences that are important for adequate molecular diagnostics, thus highlighting the importance of continuous surveillance and molecular characterization of AI viruses.